

From: Fredman, Jeffrey
 Sent: Thursday, August 18, 2005 7:37 AM
 To: STIC-Biotech/ChemLib
 Cc: Steadman, David (AU1652)
 Subject: FW: RUSH sequence request for 08/951,188

I Approve this search

PLEASE RUSH.

Jeff Fredman

-----Original Message-----

From: Steadman, David (AU1652)
 Sent: Thursday, August 18, 2005 7:37 AM
 To: Fredman, Jeffrey
 Subject: RUSH sequence request for 08/951,188

Jeff,

I would like to request the RUSH sequence request shown below. The case is in after final status and the claims are now allowable by examiner's amendment. This case was examined by another examiner before we started limiting applicants to 1 sequence and, consequently, several distinct sequences are claimed, including fragments, requiring score over length searches in addition to standard searches. Thank you very much.

David

NAME: David Steadman
 AU: 1656
 Date: 08/18/05
 Office: Remsen 2B05
 Mailbox: Remsen 3C70

Please perform the following searches in commercial and interference databases:

- 1) Standard search of SEQ ID NO:2 against nucleic acid databases (back translation).
- 2) Standard search of SEQ ID NO:6 against nucleic acid databases (back translation).
[not claimed by itself]
- 3) Score over length search of SEQ ID NO:4 against nucleic acid databases (back translation). Minimum size is 16 amino acids or 48 nucleotides. Maximum size is 1097 amino acids or 3291 nucleotides. Provide hits with 100% identity only.

 STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-
 Date Searcher Picked up: _____
 Date Completed: _____
 Searcher Prep/Rev. Time: _____
 Online Time: _____

 Type of Search

NA#: _____ AA#: _____
 Interference: _____ SPDI: _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure#: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable

STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other(Specify): _____

me

- 4) Score over length search of SEQ ID NO:45 against nucleic acid databases (back translation). Minimum size is 20 amino acids or 60 nucleotides. Maximum size is 696 amino acids or 2088 nucleotides. Provide hits with 100% identity only.
- 5) Score over length search of SEQ ID NO:47 against nucleic acid databases (back translation). Minimum size is 20 amino acids or 60 nucleotides. Maximum size is 729 amino acids or 2187 nucleotides. Provide hits with 100% identity only.
- 6) Score over length search of SEQ ID NO:50 against nucleic acid databases (back translation). Minimum size is 125 amino acids or 375 nucleotides. Maximum size is 726 amino acids or 2178 nucleotides. Provide hits with 100% identity only.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

24 August, 2005

David,

I did the Score Over Length searches on seq's 4, 45, 47, and 50, and none of them came up with a score higher than 33%, apparently too low to meet your requirements.


Mary Jane Ruhl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 09:36:48 ; Search time 817.371 Seconds
(without alignments)
3211.216 Million cell updates/sec

Title: US-08-951-188A-2
Perfect score: 2136
Sequence: 1 MAHMSHMLQQPSGSTPSNVG.....QLTTMNQKPQDNSMIDRVW 404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111320_5843/app_query.fasta_1.1102
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08951188@CGN_1_1_626@runat_18082005_111320_5843
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
No.	Score	Match	Length	DB	ID		
1	1406	65.8	1791	19	US-10-635-854A-2	Sequence 2, Appli	
2	1404	65.7	1461	10	US-09-932-257A-16	Sequence 16, Appl	
3	1404	65.7	1461	19	US-10-315-765-11	Sequence 11, Appl	
4	1385.5	64.9	1827	9	US-09-925-302-270	Sequence 270, App	
5	1385.5	64.9	1827	10	US-09-925-302-270	Sequence 270, App	
6	903.5	42.3	7018	19	US-10-315-765-4	Sequence 4, Appli	
7	824.5	38.6	1734	19	US-10-437-963-55729	Sequence 55729, A	
8	822	38.5	1755	18	US-10-425-114-27348	Sequence 27348, A	
9	822	38.5	2096	20	US-10-425-115-126873	Sequence 126873,	
10	805	37.7	1917	20	US-10-425-115-126871	Sequence 126871,	
11	801	37.5	3277	18	US-10-424-599-113880	Sequence 113880,	
12	777	36.4	1817	20	US-10-425-115-126874	Sequence 126874,	
13	739.5	34.6	5272	16	US-10-102-555-1	Sequence 1, Appli	
14	739.5	34.6	5515	15	US-10-177-293-85	Sequence 85, Appl	
15	739.5	34.6	5515	17	US-10-435-696-5	Sequence 5, Appli	
16	736.5	34.5	4336	20	US-10-370-715B-227	Sequence 227, App	
17	736.5	34.5	5590	14	US-10-198-846-13170	Sequence 13170, A	
18	736.5	34.5	6095	18	US-10-425-114-26955	Sequence 26955, A	
19	728.5	34.1	5272	22	US-10-840-512-53	Sequence 53, Appl	
20	692	32.4	1746	20	US-10-425-115-53015	Sequence 53015, A	
21	685.5	32.1	1884	19	US-10-437-963-54819	Sequence 54819, A	
c	22	652.5	30.5	4524	19	US-10-437-963-54903	Sequence 54903, A
	23	645	30.2	2123	18	US-10-425-114-33224	Sequence 33224, A
	24	645	30.2	2491	20	US-10-425-115-43609	Sequence 43609, A
	25	643.5	30.1	1547	19	US-10-767-795-3519	Sequence 3519, Ap
	26	642	30.1	1974	17	US-10-369-493-46224	Sequence 46224, A
	27	641	30.0	1587	17	US-10-369-493-45922	Sequence 45922, A
	28	641	30.0	3211	19	US-10-767-701-14646	Sequence 14646, A
	29	639	29.9	1374	20	US-10-425-115-172432	Sequence 172432,
	30	635	29.7	1703	18	US-10-425-114-13251	Sequence 13251, A
	31	632.5	29.6	1734	19	US-10-437-963-100348	Sequence 100348,
	32	629.5	29.5	2676	19	US-10-437-963-44717	Sequence 44717, A
	33	629	29.4	1805	9	US-09-964-824A-288	Sequence 288, App
	34	629	29.4	1805	21	US-10-843-641A-5591	Sequence 5591, Ap
	35	629	29.4	2471	9	US-09-915-060-3	Sequence 3, Appli
	36	628	29.4	3863	9	US-09-964-824A-283	Sequence 283, App
	37	628	29.4	3863	21	US-10-843-641A-5586	Sequence 5586, Ap
	38	628	29.4	3883	15	US-10-037-270-792	Sequence 792, App
	39	628	29.4	3883	17	US-10-117-722-792	Sequence 792, App
c	40	627.5	29.4	2803	19	US-10-437-963-12796	Sequence 12796, A
	41	627	29.4	2021	20	US-10-425-115-153767	Sequence 153767,
	42	625.5	29.3	1913	22	US-10-704-513-5	Sequence 5, Appli
	43	624	29.2	2511	18	US-10-425-114-6377	Sequence 6377, Ap
	44	623.5	29.2	1883	14	US-10-081-119-21	Sequence 21, Appli
	45	623.5	29.2	1883	21	US-10-951-389-21	Sequence 21, Appli

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 04:38:55 ; Search time 4254.49 Seconds
(without alignments)
3614.522 Million cell updates/sec

Title: US-08-951-188A-2
Perfect score: 2136
Sequence: 1 MAHMSHMLQQPSGSTPSNVG.....QQLTTMNQKPQDNSMIDRVW 404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111318_5747/app_query.fasta_1.1102
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_4385@runat_18082005_111318_5747 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1406	65.8	1222	3	CR619508	CR619508 full-leng
2	1406	65.8	1761	3	CR618153	CR618153 full-leng
3	1290	60.4	1027	9	AY407322	AY407322 Homo sapi
4	1289	60.3	1566	3	AK089276	AK089276 Mus muscu
5	1286	60.2	1027	9	AY407324	AY407324 Mus muscu
6	1256	58.8	965	3	CNS08E51	BX007745 Single re
7	1248	58.4	899	3	CNS08S57	BX025895 Single re
8	1248	58.4	959	3	CNS08YRM	BX034478 Single re

9	1246	58.3	819	3	CNS08PI2	BX022470 Single re
10	1241	58.1	1027	9	AY407323	AY407323 Pan trogl
11	1224.5	57.3	905	7	CN586484	CN586484 USDA-FF_1
12	1223.5	57.3	848	6	CD791177	CD791177 EST662538
c 13	1205	56.4	982	3	CNS08YRN	BX034479 Single re
c 14	1204.5	56.4	979	5	BX364596	BX364596 BX364596
15	1173.5	54.9	958	5	BX364597	BX364597 BX364597
16	1152.5	54.0	1059	5	BX355158	BX355158 BX355158
17	1152.5	54.0	1070	5	BX384777	BX384777 BX384777
18	1143	53.5	666	4	BI354233	BI354233 GM15595.5
19	1135	53.1	821	7	CR589672	CR589672 CR589672
c 20	1134	53.1	955	3	CNS08PI3	BX022471 Single re
21	1133.5	53.1	1055	5	BX355377	BX355377 BX355377
22	1131.5	53.0	1106	5	BX353798	BX353798 BX353798
23	1126.5	52.7	1168	5	BU510098	BU510098 AGENCOURT
24	1119.5	52.4	899	5	BX374660	BX374660 BX374660
25	1117.5	52.3	925	4	BI409756	BI409756 602963091
26	1116.5	52.3	1182	5	BU515351	BU515351 AGENCOURT
27	1111	52.0	704	4	BI640898	BI640898 SD23923.5
c 28	1096	51.3	967	3	CNS08E52	BX007746 Single re
29	1081	50.6	817	1	AA390634	AA390634 LD09645.5
30	1073.5	50.3	845	7	CK870426	CK870426 AGENCOURT
31	1068	50.0	671	1	AI518481	AI518481 LD38011.5
32	1066.5	49.9	852	4	BI412108	BI412108 602964859
33	1056	49.4	665	5	BQ785080	BQ785080 Ae4-403 4
34	1050.5	49.2	828	5	BX331346	BX331346 BX331346
35	1045	48.9	706	4	BM605073	BM605073 170006870
36	1044.5	48.9	886	5	BQ877844	BQ877844 AGENCOURT
37	1037	48.5	649	1	AI513433	AI513433 LD45702.5
38	1035	48.5	817	5	BM949049	BM949049 UI-M-EM0-
39	1027.5	48.1	839	7	CN176915	CN176915 AGENCOURT
40	1026	48.0	748	7	CF951488	CF951488 UI-M-HL0-
41	1018.5	47.7	826	1	AJ456950	AJ456950 AJ456950
42	1015	47.5	676	4	BI214314	BI214314 RE20085.5
43	1010.5	47.3	796	7	CK018197	CK018197 AGENCOURT
44	1007.5	47.2	865	5	BQ436563	BQ436563 AGENCOURT
45	1007	47.1	824	7	CO555395	CO555395 AGENCOURT

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 02:04:13 ; Search time 5759.08 Seconds
(without alignments)
3399.136 Million cell updates/sec

Title: US-08-951-188A-2
Perfect score: 2136
Sequence: 1 MAHMSHMLQQPSGSTPSNVG.....QQLTTMNQKPQDNSMIDRVW 404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111317_5733/app_query.fasta_1.1102
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_5970@runat_18082005_111317_5733 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	2136	100.0	1447	6	CQ582909	CQ582909 Sequence
2	2136	100.0	1457	3	AF027300	AF027300 Drosophil
3	2136	100.0	1479	3	AY118809	AY118809 Drosophil

c	4	2002	93.7	3636	6	CQ582908	CQ582908 Sequence
c	5	2002	93.7	78277	2	AC020206	AC020206 Drosophil
	6	2002	93.7	81677	3	AC004377	AC004377 Drosophil
c	7	2002	93.7	169534	3	AC008350	AC008350 Drosophil
c	8	2002	93.7	302225	3	AE003458	AE003458 Drosophil
	9	1457.5	68.2	1768	5	AF268046	AF268046 <i>Danio rer</i>
	10	1444.5	67.6	1732	5	BC055634	BC055634 <i>Danio rer</i>
	11	1424	66.7	1601	5	CR762201	CR762201 <i>Xenopus t</i>
	12	1424	66.7	1802	5	BC074560	BC074560 <i>Xenopus t</i>
	13	1414	66.2	1836	5	BC045247	BC045247 <i>Xenopus l</i>
	14	1413.5	66.2	2513	5	AJ720053	AJ720053 <i>Gallus ga</i>
	15	1406	65.8	1753	9	BC001968	BC001968 <i>Homo sapi</i>
	16	1404	65.7	1461	6	AR136816	AR136816 Sequence
	17	1404	65.7	1461	6	I68138	I68138 Sequence 1
	18	1404	65.7	1461	9	HUMCDCTR	L25676 <i>Homo sapien</i>
	19	1400	65.5	1459	6	CQ717109	CQ717109 Sequence
	20	1400	65.5	1758	9	HSSTPKC2K	X80230 <i>H.sapiens m</i>
	21	1399	65.5	1119	12	AY335628	AY335628 Synthetic
	22	1391	65.1	1644	10	AF327431	AF327431 <i>Mus muscu</i>
	23	1391	65.1	1710	10	BC003901	BC003901 <i>Mus muscu</i>
	24	1389	65.0	1699	10	BC082037	BC082037 <i>Rattus no</i>
	25	1359	63.6	1347	3	AK114703	AK114703 <i>Ciona int</i>
c	26	1225	57.4	3854	6	CQ598463	CQ598463 Sequence
	27	927	43.4	5572	9	AF255306	AF255306 <i>Homo sapi</i>
	28	903.5	42.3	6333	9	AF517840	AF517840 <i>Homo sapi</i>
	29	903.5	42.3	80642	9	AL162586	AL162586 Human DNA
	30	897.5	42.0	216765	2	AC142126	AC142126 <i>Rattus no</i>
c	31	897	42.0	3013	6	CQ580481	CQ580481 Sequence
	32	829	38.8	1827	8	LES294903	AJ294903 <i>Lycopersi</i>
	33	826	38.7	5719	10	AF327569	AF327569 <i>Mus muscu</i>
c	34	826	38.7	204136	10	AL772271	AL772271 Mouse DNA
c	35	826	38.7	204407	2	AC021446	AC021446 <i>Mus muscu</i>
	36	819.5	38.4	1870	8	AK103469	AK103469 <i>Oryza sat</i>
	37	817.5	38.3	1878	8	AK073808	AK073808 <i>Oryza sat</i>
	38	805	37.7	1876	6	AX041002	AX041002 Sequence
	39	802.5	37.6	1772	8	BT014075	BT014075 <i>Lycopersi</i>
	40	797.5	37.3	1856	8	BT002565	BT002565 <i>Arabidops</i>
	41	797.5	37.3	1856	8	AY062449	AY062449 <i>Arabidops</i>
	42	797	37.3	1789	8	MSCDC2MSC	X97314 <i>M.sativa mR</i>
	43	795.5	37.2	1542	8	AY039990	AY039990 <i>Arabidops</i>
	44	795.5	37.2	1862	8	AF360134	AF360134 <i>Arabidops</i>
	45	794.5	37.2	1848	8	OSA564977	AJ564977 <i>Oryza sat</i>

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 05:41:46 ; Search time 219.18 Seconds
(without alignments)
3016.035 Million cell updates/sec

Title: US-08-951-188A-2
Perfect score: 2136
Sequence: 1 MAHMSSHMLQQPSGSTPSNVG.....QQLTTMNQKPQDNSMIDRVW 404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111319_5757/app_query.fasta_1.1102
-DB=Issued_Patents_NA -QFORMAT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFORMAT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_93@runat_18082005_111319_5757 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1404	65.7	1461	1	US-08-403-634-1	Sequence 1, Appli
2	1404	65.7	1461	3	US-08-913-441B-1	Sequence 1, Appli
3	1404	65.7	1461	4	US-09-571-985C-1	Sequence 1, Appli
4	1400	65.5	1459	4	US-09-949-016-5837	Sequence 5837, Ap
5	897.5	42.0	7736	4	US-09-949-016-17579	Sequence 17579, A
6	725.5	34.0	2224	4	US-09-949-016-5652	Sequence 5652, Ap
7	725.5	34.0	2224	4	US-09-949-016-5653	Sequence 5653, Ap
8	648	30.3	1680	4	US-09-248-796A-4378	Sequence 4378, Ap
9	631	29.5	2422	4	US-09-949-016-3805	Sequence 3805, Ap
10	629	29.4	2471	4	US-09-915-060A-3	Sequence 3, Appli
11	628	29.4	3883	4	US-09-620-312D-792	Sequence 792, App

12	621.5	29.1	3505	1	US-07-660-465-1	Sequence 1, Appli
13	618	28.9	993	4	US-09-248-796A-4323	Sequence 4323, Ap
14	618	28.9	1002	1	US-08-463-090B-3	Sequence 3, Appli
15	616.5	28.9	1424	1	US-08-403-634-3	Sequence 3, Appli
16	616.5	28.9	1424	3	US-08-913-441B-3	Sequence 3, Appli
17	616.5	28.9	1424	4	US-09-571-985C-3	Sequence 3, Appli
18	605	28.3	1158	4	US-09-949-016-4906	Sequence 4906, Ap
19	604	28.3	1161	4	US-09-023-655-1373	Sequence 1373, Ap
20	604	28.3	1161	4	US-09-949-016-181	Sequence 181, App
21	604	28.3	1825	4	US-09-620-312D-313	Sequence 313, APP
22	602.5	28.2	1635	4	US-09-417-197-112	Sequence 112, App
23	600.5	28.1	1476	2	US-08-969-106-1	Sequence 1, Appli
24	600.5	28.1	1476	4	US-09-338-125-1	Sequence 1, Appli
25	600.5	28.1	1476	4	US-09-266-225D-13	Sequence 13, Appl
26	600.5	28.1	1635	4	US-09-417-197-114	Sequence 114, App
27	597.5	28.0	1296	4	US-09-949-016-2154	Sequence 2154, Ap
28	597.5	28.0	2213	4	US-09-023-655-1037	Sequence 1037, Ap
29	595.5	27.9	1666	4	US-09-949-016-5677	Sequence 5677, Ap
30	594	27.8	1050	4	US-09-220-132-3	Sequence 3, Appli
31	593	27.8	2868	4	US-09-620-312D-53	Sequence 53, Appl
32	589	27.6	1042	4	US-09-949-016-4802	Sequence 4802, Ap
33	584.5	27.4	1242	4	US-09-016-434-1283	Sequence 1283, Ap
34	583.5	27.3	3111	4	US-09-695-795A-7	Sequence 7, Appli
35	583.5	27.3	3111	4	US-09-695-795A-21	Sequence 21, Appl
36	581	27.2	1825	4	US-09-919-039-115	Sequence 115, App
37	579	27.1	903	2	US-08-874-347-9	Sequence 9, Appli
38	579	27.1	903	3	US-09-093-522-9	Sequence 9, Appli
39	578	27.1	999	4	US-09-248-796A-4296	Sequence 4296, Ap
40	576	27.0	1089	1	US-08-154-915-1	Sequence 1, Appli
41	576	27.0	1089	2	US-08-464-517-37	Sequence 37, Appl
42	576	27.0	1089	2	US-08-246-361A-37	Sequence 37, Appl
43	576	27.0	1089	3	US-08-463-772-37	Sequence 37, Appl
44	576	27.0	1089	5	PCT-US93-09945-1	Sequence 1, Appli
45	575.5	26.9	987	4	US-09-949-016-5854	Sequence 5854, Ap

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 01:57:22 ; Search time 689.299 Seconds
(without alignments)
3469.576 Million cell updates/sec

Title: US-08-951-188A-2
Perfect score: 2136
Sequence: 1 MAHMSHMLQQPSGSTPSNVG.....QLTTMNQKPQDNSMIDRVW 404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111317_5725/app_query.fasta_1.1102
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_586@runat_18082005_111317_5725 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2136	100.0	1447	4	ABL08951	Abl08951 Drosophil
c	2	2002	93.7	3636	4	ABL08950
3	1406	65.8	1791	12	AD014235	Ado14235 Human CDK
4	1404	65.7	1460	2	AAT38075	Aat38075 Sequence

5	1404	65.7	1461	9	ACD26032	Acd26032 Human cDN	
6	1404	65.7	1461	12	ADP74227	Adp74227 Human cyc	
7	1385.5	64.9	1827	3	AAF18251	Aaf18251 Lung canc	
c	8	1225	57.4	3854	4	ABL19320	Abl19320 Drosophil
9	1202.5	56.3	1046	12	ADK71936	Adk71936 Human kin	
10	903.5	42.3	7018	12	ADP74220	Adp74220 Human cyc	
c	11	897	42.0	3013	4	ABL07332	Abl07332 Drosophil
12	805	37.7	1876	3	AAC83113	Aac83113 DNA encod	
13	794	37.2	1518	12	ADN72460	Adn72460 Thale cre	
14	794	37.2	1738	11	ADP09870	Adp09870 Plant CDK	
15	739.5	34.6	4473	4	AAF44671	Aaf44671 Novel pro	
16	739.5	34.6	4473	12	ADI29369	Adi29369 Human MAR	
17	739.5	34.6	4574	4	AAK52124	Aak52124 Human pol	
18	739.5	34.6	5272	12	ADH29596	Adh29596 Human Crk	
19	739.5	34.6	5451	10	ADD89962	Add89962 Human can	
20	739.5	34.6	5515	8	ACC50119	Acc50119 Breast ca	
21	739.5	34.6	5515	12	ADH13156	Adh13156 Human mal	
22	738	34.6	4179	4	ABL13069	Abl13069 Drosophil	
23	736.5	34.5	4336	10	ADF76553	Adf76553 Novel hum	
24	736.5	34.5	5590	11	ACN92020	Acn92020 Breast ca	
25	732.5	34.3	3387	4	AAK53108	Aak53108 Human pol	
c	26	721.5	33.8	4029	5	AAS84145	Aas84145 DNA encod
27	713	33.4	5063	12	ADK71887	Adk71887 Human kin	
28	652	30.5	6905	4	ABL13068	Abl13068 Drosophil	
29	643.5	30.1	1547	13	ADR62738	Adr62738 Cotton cD	
30	642	30.1	1974	10	ACC61483	Acc61483 Gene sequ	
31	642	30.1	1974	10	ADK64643	Adk64643 Disease t	
32	642	30.1	1974	13	ADT47786	Adt47786 Bacterial	
33	641	30.0	1587	10	ACC61829	Acc61829 Gene sequ	
34	641	30.0	1587	10	ADK63787	Adk63787 Disease t	
35	641	30.0	1587	13	ADT47484	Adt47484 Bacterial	
36	634	29.7	2213	2	AAQ02263	Aaq02263 cDNA sequ	
37	631	29.5	2439	10	ADG32915	Adg32915 Human DNA	
38	631	29.5	2969	10	ADG74710	Adg74710 Human kin	
39	631	29.5	3324	13	ACN42355	Acn42355 Human dia	
40	631	29.5	3593	13	ACN42354	Acn42354 Human dia	
41	629	29.4	1805	6	ABL67254	Abl67254 Thyroid c	
42	629	29.4	2471	3	AAA73711	Aaa73711 Human PIT	
43	629	29.4	2471	3	ABL51630	Abl51630 Human PIT	
44	628	29.4	3863	6	ABL67249	Abl67249 Thyroid c	
45	628	29.4	3883	4	AAI58900	Aai58900 Human pol	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 05:41:46 ; Search time 201.82 Seconds
(without alignments)
3016.035 Million cell updates/sec

Title: US-08-951-188A-6
Perfect score: 1951
Sequence: 1 MAKQYDSVECPFCDEVSKYE.....STNQSRNPATTNQTEFERVF 372

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111319_5757/app_query.fasta_1.1102
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_93@runat_18082005_111319_5757 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1951	100.0	1461	1	US-08-403-634-1	Sequence 1, Appli
2	1951	100.0	1461	3	US-08-913-441B-1	Sequence 1, Appli
3	1951	100.0	1461	4	US-09-571-985C-1	Sequence 1, Appli
4	1945	99.7	1459	4	US-09-949-016-5837	Sequence 5837, Ap
5	1394	71.5	7736	4	US-09-949-016-17579	Sequence 17579, A
6	755.5	38.7	2224	4	US-09-949-016-5652	Sequence 5652, Ap
7	755.5	38.7	2224	4	US-09-949-016-5653	Sequence 5653, Ap
8	680.5	34.9	1680	4	US-09-248-796A-4378	Sequence 4378, Ap
9	599	30.7	1424	1	US-08-403-634-3	Sequence 3, Appli
10	599	30.7	1424	3	US-08-913-441B-3	Sequence 3, Appli
11	599	30.7	1424	4	US-09-571-985C-3	Sequence 3, Appli

12	592.5	30.4	2422	4	US-09-949-016-3805	Sequence 3805, Ap
13	590.5	30.3	1050	4	US-09-220-132-3	Sequence 3, Appli
14	590.5	30.3	2471	4	US-09-915-060A-3	Sequence 3, Appli
15	589.5	30.2	3883	4	US-09-620-312D-792	Sequence 792, App
16	587.5	30.1	3505	1	US-07-660-465-1	Sequence 1, Appli
17	585.5	30.0	1042	4	US-09-949-016-4802	Sequence 4802, Ap
18	580.5	29.8	1825	4	US-09-919-039-115	Sequence 115, App
19	576.5	29.5	993	4	US-09-248-796A-4323	Sequence 4323, Ap
20	576.5	29.5	1002	1	US-08-463-090B-3	Sequence 3, Appli
21	576	29.5	1666	4	US-09-949-016-5677	Sequence 5677, Ap
22	573.5	29.4	987	4	US-09-949-016-5854	Sequence 5854, Ap
23	571.5	29.3	1158	4	US-09-949-016-4906	Sequence 4906, Ap
24	571.5	29.3	1161	4	US-09-023-655-1373	Sequence 1373, Ap
25	571.5	29.3	1161	4	US-09-949-016-181	Sequence 181, App
26	571.5	29.3	1825	4	US-09-620-312D-313	Sequence 313, App
27	570.5	29.2	2868	4	US-09-620-312D-53	Sequence 53, Appli
28	568	29.1	3111	4	US-09-695-795A-7	Sequence 7, Appli
29	568	29.1	3111	4	US-09-695-795A-21	Sequence 21, Appli
30	564.5	28.9	903	2	US-08-874-347-9	Sequence 9, Appli
31	564.5	28.9	903	3	US-09-093-522-9	Sequence 9, Appli
32	564.5	28.9	1089	1	US-08-154-915-1	Sequence 1, Appli
33	564.5	28.9	1089	2	US-08-464-517-37	Sequence 37, Appli
34	564.5	28.9	1089	2	US-08-246-361A-37	Sequence 37, Appli
35	564.5	28.9	1089	3	US-08-463-772-37	Sequence 37, Appli
36	564.5	28.9	1089	5	PCT-US93-09945-1	Sequence 1, Appli
37	562.5	28.8	1476	2	US-08-969-106-1	Sequence 1, Appli
38	562.5	28.8	1476	4	US-09-338-125-1	Sequence 1, Appli
39	562.5	28.8	1476	4	US-09-266-225D-13	Sequence 13, Appli
40	562	28.8	1635	4	US-09-417-197-112	Sequence 112, App
41	562	28.8	1635	4	US-09-417-197-114	Sequence 114, App
42	558	28.6	1296	4	US-09-949-016-2154	Sequence 2154, Ap
43	558	28.6	2213	4	US-09-023-655-1037	Sequence 1037, Ap
44	551.5	28.3	999	4	US-09-248-796A-4296	Sequence 4296, Ap
45	547.5	28.1	1242	4	US-09-016-434-1283	Sequence 1283, Ap

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 04:38:55 ; Search time 3917.51 Seconds
(without alignments)
3614.522 Million cell updates/sec

Title: US-08-951-188A-6
Perfect score: 1951
Sequence: 1 MAKQYDSVECPFCDEVSKYE.....STNQSRNPATTNQTEFERVF 372

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111318_5747/app_query.fasta_1.1102
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188 @CGN_1_1_4385 @runat_18082005_111318_5747 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1951	100.0	1222	3	CR619508	CR619508 full-leng
2	1951	100.0	1761	3	CR618153	CR618153 full-leng
3	1777	91.1	1027	9	AY407322	AY407322 Homo sapi
4	1766	90.5	1027	9	AY407324	AY407324 Mus muscu
5	1766	90.5	1566	3	AK089276	AK089276 Mus muscu
6	1719	88.1	1027	9	AY407323	AY407323 Pan trogl
c	1648	84.5	979	5	BX364596	BX364596 BX364596
8	1599.5	82.0	1168	5	BU510098	BU510098 AGENCOURT

9	1541	79.0	1182	5	BU515351	BU515351 AGENCOURT
10	1528	78.3	958	5	BX364597	BX364597 BX364597
11	1485	76.1	1106	5	BX353798	BX353798 BX353798
12	1474.5	75.6	1070	5	BX384777	BX384777 BX384777
13	1470	75.3	1059	5	BX355158	BX355158 BX355158
14	1457	74.7	1055	5	BX355377	BX355377 BX355377
15	1432	73.4	899	5	BX374660	BX374660 BX374660
16	1422.5	72.9	925	4	BI409756	BI409756 602963091
17	1338	68.6	886	5	BQ877844	BQ877844 AGENCOURT
18	1326.5	68.0	852	4	BI412108	BI412108 602964859
19	1325	67.9	821	7	CR589672	CR589672 CR589672
20	1314	67.4	828	5	BX331346	BX331346 BX331346
21	1293	66.3	748	7	CF951488	CF951488 UI-M-HU0-
22	1286	65.9	817	5	BM949049	BM949049 UI-M-EM0-
23	1267	64.9	865	5	BQ436563	BQ436563 AGENCOURT
24	1251	64.1	826	5	BP436206	BP436206 BP436206
25	1249	64.0	824	7	CO555395	CO555395 AGENCOURT
26	1247	63.9	846	7	CN539794	CN539794 UI-M-HU0-
27	1243	63.7	826	1	AJ456950	AJ456950 AJ456950
28	1235	63.3	707	7	CK834404	CK834404 4058845 B
29	1234	63.2	727	4	BI834687	BI834687 603090468
30	1230	63.0	905	7	CN156541	CN156541 943947 MA
31	1229	63.0	869	4	BI101143	BI101143 602886828
32	1225	62.8	848	6	CD791177	CD791177 EST662538
33	1224	62.7	964	2	BE313097	BE313097 601153840
34	1222	62.6	785	7	CK477489	CK477489 AGENCOURT
35	1216	62.3	830	1	AI040910	AI040910 ow26c10.x
36	1206	61.8	876	4	BM459554	BM459554 AGENCOURT
37	1205	61.8	698	7	CN789021	CN789021 4123426 B
38	1204	61.7	845	7	CK870426	CK870426 AGENCOURT
39	1197	61.4	884	5	BQ232229	BQ232229 AGENCOURT
40	1190.5	61.0	996	4	BI414563	BI414563 602986132
41	1185	60.7	915	5	BU148882	BU148882 AGENCOURT
42	1181.5	60.6	1146	4	BI253887	BI253887 602974672
43	1171	60.0	698	7	CK941635	CK941635 4065197 B
44	1170.5	60.0	902	5	BU552837	BU552837 AGENCOURT
45	1153	59.1	857	4	BI852673	BI852673 603379332

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 09:36:48 ; Search time 752.629 Seconds
(without alignments)
3211.216 Million cell updates/sec

Title: US-08-951-188A-6
Perfect score: 1951
Sequence: 1 MAKQYDSVECPFCDEVSKYE.....STNQSRNPATTNQTEFERVF 372

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111320_5843/app_query.fasta_1.1102
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08951188@CGN_1_1_626@runat_18082005_111320_5843
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1951	100.0	1461	10	US-09-932-257A-16	Sequence 16, Appl
2	1951	100.0	1461	19	US-10-315-765-11	Sequence 11, Appl
3	1951	100.0	1791	19	US-10-635-854A-2	Sequence 2, Appli
4	1924	98.6	1827	9	US-09-925-302-270	Sequence 270, App
5	1924	98.6	1827	10	US-09-925-302-270	Sequence 270, App
6	1412	72.4	7018	19	US-10-315-765-4	Sequence 4, Appli
7	955.5	49.0	1269	9	US-09-771-161A-21	Sequence 21, Appl
8	827	42.4	1734	19	US-10-437-963-55729	Sequence 55729, A
9	815.5	41.8	1755	18	US-10-425-114-27348	Sequence 27348, A
10	815.5	41.8	2096	20	US-10-425-115-126873	Sequence 126873,
11	813	41.7	3277	18	US-10-424-599-113880	Sequence 113880,
12	808.5	41.4	1917	20	US-10-425-115-126871	Sequence 126871,
c 13	783.5	40.2	60367	19	US-10-322-281-372	Sequence 372, App
14	773.5	39.6	1817	20	US-10-425-115-126874	Sequence 126874,
15	769	39.4	5272	16	US-10-102-555-1	Sequence 1, Appli
16	767	39.3	5515	15	US-10-177-293-85	Sequence 85, Appl
17	767	39.3	5515	17	US-10-435-696-5	Sequence 5, Appli
18	764	39.2	4336	20	US-10-370-715B-227	Sequence 227, App
19	764	39.2	5590	14	US-10-198-846-13170	Sequence 13170, A
20	764	39.2	6095	18	US-10-425-114-26955	Sequence 26955, A
21	754	38.6	5272	22	US-10-840-512-53	Sequence 53, Appl
22	702	36.0	1884	19	US-10-437-963-54819	Sequence 54819, A
23	686	35.2	405	9	US-09-796-692-2980	Sequence 2980, Ap
24	686	35.2	405	14	US-10-040-862-2980	Sequence 2980, Ap
25	686	35.2	405	17	US-10-057-475B-2980	Sequence 2980, Ap
26	686	35.2	405	17	US-10-154-884B-2980	Sequence 2980, Ap
27	686	35.2	405	19	US-10-764-324-2980	Sequence 2980, Ap
28	672	34.4	1746	20	US-10-425-115-53015	Sequence 53015, A
29	668	34.2	1374	20	US-10-425-115-172432	Sequence 172432,
30	640.5	32.8	1734	19	US-10-437-963-100348	Sequence 100348,
31	639.5	32.8	560	16	US-10-029-386-3104	Sequence 3104, Ap
32	639.5	32.8	2210	20	US-10-425-115-153769	Sequence 153769,
33	637	32.6	370	16	US-10-029-386-16804	Sequence 16804, A
34	635.5	32.6	1587	17	US-10-369-493-45922	Sequence 45922, A
35	635.5	32.6	2123	18	US-10-425-114-33224	Sequence 33224, A
36	635.5	32.6	2491	20	US-10-425-115-43609	Sequence 43609, A
37	634.5	32.5	2021	20	US-10-425-115-153767	Sequence 153767,
38	631.5	32.4	3211	19	US-10-767-701-14646	Sequence 14646, A
39	631	32.3	1469	19	US-10-437-963-70330	Sequence 70330, A
c 40	626.5	32.1	4524	19	US-10-437-963-54903	Sequence 54903, A
41	623.5	32.0	1725	19	US-10-437-963-70491	Sequence 70491, A
42	619.5	31.8	1547	19	US-10-767-795-3519	Sequence 3519, App
43	618	31.7	3855	17	US-10-260-238-691	Sequence 691, App
44	618	31.7	5922	19	US-10-437-963-40613	Sequence 40613, A
45	616	31.6	2501	20	US-10-425-115-30518	Sequence 30518, A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 01:57:22 ; Search time 634.701 Seconds
(without alignments)
3469.576 Million cell updates/sec

Title: US-08-951-188A-6
Perfect score: 1951
Sequence: 1 MAKQYDSVECPFCDEVSKYE.....STNQSRNPATTNQTEFERVF 372

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111317_5725/app_query.fasta_1.1102
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_586@runat_18082005_111317_5725 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
<hr/>							
1	1951	100.0	1460	2	AAT38075		Aat38075 Sequence
2	1951	100.0	1461	9	ACD26032		Acd26032 Human cDN
3	1951	100.0	1461	12	ADP74227		Adp74227 Human cyc
4	1951	100.0	1791	12	ADO14235		Ado14235 Human CDK

5	1924	98.6	1827	3	AAF18251	Aaf18251 Lung canc
6	1741.5	89.3	1046	12	ADK71936	Adk71936 Human kin
7	1412	72.4	7018	12	ADP74220	Adp74220 Human cyc
8	1399.5	71.7	1447	4	ABL08951	Abl08951 Drosophil
c 9	1265.5	64.9	3636	4	ABL08950	Abl08950 Drosophil
c 10	851	43.6	3854	4	ABL19320	Abl19320 Drosophil
11	819.5	42.0	1518	12	ADN72460	Adn72460 Thale cre
12	819.5	42.0	1738	11	ADP09870	Adp09870 Plant CDK
13	808.5	41.4	1876	3	AAC83113	Aac83113 DNA encod
c 14	783.5	40.2	60367	13	ABD33309	Abd33309 Human can
15	769	39.4	5272	12	ADH29596	Adh29596 Human Crk
16	767	39.3	4473	4	AAF44671	Aaf44671 Novel pro
17	767	39.3	4473	12	ADI29369	Adi29369 Human MAR
18	767	39.3	4574	4	AAK52124	Aak52124 Human pol
19	767	39.3	5451	10	ADD89962	Add89962 Human can
20	767	39.3	5515	8	ACC50119	Acc50119 Breast ca
21	767	39.3	5515	12	ADH13156	Adh13156 Human mal
22	766.5	39.3	4179	4	ABL13069	Abl13069 Drosophil
23	764	39.2	4336	10	ADF76553	Adf76553 Novel hum
24	764	39.2	5590	11	ACN92020	Acn92020 Breast ca
25	760	39.0	3387	4	AAK53108	Aak53108 Human pol
26	754	38.6	5063	12	ADK71887	Adk71887 Human kin
c 27	749	38.4	4029	5	AAS84145	Aas84145 DNA encod
28	685	35.1	6905	4	ABL13068	Abl13068 Drosophil
29	639.5	32.8	560	12	ACH69909	Ach69909 Human gen
30	637.5	32.7	2213	2	AAQ02263	Aaq02263 cDNA sequ
31	637	32.6	370	12	ACH83609	Ach83609 Human gen
32	635.5	32.6	1587	10	ACC61829	Acc61829 Gene sequ
33	635.5	32.6	1587	10	ADK63787	Adk63787 Disease t
34	635.5	32.6	1587	13	ADT47484	Adt47484 Bacterial
35	632.5	32.4	2111	12	ADN05478	Adn05478 Antipsori
36	619.5	31.8	1547	13	ADR62738	Adr62738 Cotton cD
37	618	31.7	3855	12	ADJ39691	Adj39691 Plant cDN
38	612.5	31.4	2089	10	ADF38056	Adf38056 Synchroni
39	607	31.1	1974	10	ACC61483	Acc61483 Gene sequ
40	607	31.1	1974	10	ADK64643	Adk64643 Disease t
41	607	31.1	1974	13	ADT47786	Adt47786 Bacterial
42	604	31.0	1656	13	ADS49347	Ads49347 Bacterial
c 43	603	30.9	1863	5	AAS88684	Aas88684 DNA encod
44	603	30.9	1883	6	ABV73991	Abv73991 Human CDC
45	603	30.9	1883	9	ACA62267	Aca62267 Human DNA

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2005, 02:04:13 ; Search time 5302.92 Seconds
(without alignments)
3399.136 Million cell updates/sec

Title: US-08-951-188A-6
Perfect score: 1951
Sequence: 1 MAKQYDSVECPFCDEVSKYE.....STNQSRNPATTNQTEFERVF 372

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US08951188/runat_18082005_111317_5733/app_query.fasta_1.1102
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08951188@CGN_1_1_5970@runat_18082005_111317_5733 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	1951	100.0	1119	12	AY335628	AY335628 Synthetic
2	1951	100.0	1461	6	AR136816	AR136816 Sequence
3	1951	100.0	1461	6	I68138	I68138 Sequence 1

4	1951	100.0	1461	9	HUMCDCTRK	L25676 Homo sapien	
5	1951	100.0	1753	9	BC001968	BC001968 Homo sapi	
6	1945	99.7	1459	6	CQ717109	CQ717109 Sequence	
7	1945	99.7	1758	9	HSSTPKC2K	X80230 H.sapiens m	
8	1931	99.0	1644	10	AF327431	AF327431 Mus muscu	
9	1931	99.0	1699	10	BC082037	BC082037 Rattus no	
10	1931	99.0	1710	10	BC003901	BC003901 Mus muscu	
11	1833	94.0	2513	5	AJ720053	AJ720053 Gallus ga	
12	1776	91.0	1601	5	CR762201	CR762201 Xenopus t	
13	1776	91.0	1802	5	BC074560	BC074560 Xenopus t	
14	1752	89.8	1768	5	AF268046	AF268046 Danio rer	
15	1741	89.2	1732	5	BC055634	BC055634 Danio rer	
16	1738	89.1	1836	5	BC045247	BC045247 Xenopus l	
17	1444	74.0	1347	3	AK114703	AK114703 Ciona int	
18	1438.5	73.7	5572	9	AF255306	AF255306 Homo sapi	
19	1412	72.4	80642	9	AL162586	AL162586 Human DNA	
20	1399.5	71.7	1447	6	CQ582909	CQ582909 Sequence	
21	1399.5	71.7	1457	3	AF027300	AF027300 Drosophil	
22	1399.5	71.7	1479	3	AY118809	AY118809 Drosophil	
23	1391.5	71.3	6333	9	AF517840	AF517840 Homo sapi	
24	1332	68.3	216765	2	AC142126	AC142126 Rattus no	
c	25	1265.5	64.9	3636	6	CQ582908	CQ582908 Sequence
c	26	1265.5	64.9	78277	2	AC020206	AC020206 Drosophil
c	27	1265.5	64.9	81677	3	AC004377	AC004377 Drosophil
c	28	1265.5	64.9	169534	3	AC008350	AC008350 Drosophil
c	29	1265.5	64.9	302225	3	AE003458	AE003458 Drosophil
c	30	1258.5	64.5	5719	10	AF327569	AF327569 Mus muscu
c	31	1258.5	64.5	204136	10	AL772271	AL772271 Mouse DNA
c	32	1258.5	64.5	204407	2	AC021446	AC021446 Mus muscu
c	33	851	43.6	3854	6	CQ598463	CQ598463 Sequence
34	826.5	42.4	1827	8	LES294903	AJ294903 Lycopersi	
35	819.5	42.0	1518	6	CQ803944	CQ803944 Sequence	
36	819.5	42.0	1518	8	AY120690	AY120690 Arabidops	
37	819.5	42.0	1717	8	AF375437	AF375437 Arabidops	
38	819.5	42.0	1738	6	AX741236	AX741236 Sequence	
39	816.5	41.9	1856	8	BT002565	BT002565 Arabidops	
40	816.5	41.9	1856	8	AY062449	AY062449 Arabidops	
41	815	41.8	1878	8	AK073808	AK073808 Oryza sat	
42	814.5	41.7	1542	8	AY039990	AY039990 Arabidops	
43	814.5	41.7	1862	8	AF360134	AF360134 Arabidops	
44	813	41.7	1870	8	AK103469	AK103469 Oryza sat	
45	808.5	41.4	1876	6	AX041002	AX041002 Sequence	